CLAIMS

We Claim:

1. A method for selecting a chromosome-specific oligonucleotide sequence, comprising:

a. identifying a chromosome-specific genic sequence that is unique in a genome;

b. identifying an exon tag sequence within said genic sequence, wherein said exon tag sequence is compared to said genome to determine that said exon tag sequence is unique within said genome, and

c. selecting an oligonucleotide sequence complementary to said exon tag or its complement.

2. The method of Claim 1, wherein said exon tag sequence within said genic sequence is less than 100 base pairs in length.

3. The method of Claim 2, wherein said exon tag sequence within said genic sequence is 91 base pairs in length.

4. The method of Claim 1, wherein said exon tag sequence is the length of an entire exon.

5. The method of Claim 1, wherein said selecting an oligonucleotide sequence complementary to said exon tag or its complement comprises selecting an oligonucleotide sequence having 20% to 70% GC content.

6. A method for detecting aneuploidy of a chromosome in a subject, comprising the steps of:

a. selecting an exon tag sequence for said chromosome;

b. providing a non-amplifying oligonucleotide detection assay configured to detect said exon tag sequence or its complement; and

c. detecting said exon tag with said non-amplifying oligonucleotide detection assay.

7. The method of Claim 6, wherein said selecting an exon tag sequence comprises the steps of:

a. identifying a genic sequence that is specific to said chromosome in said subject, and that is unique in the genome of the species of said subject;

b. identifying an exon tag sequence within said genic sequence, wherein said exon tag sequence is compared to said genome to determine that said exon tag sequence is unique within said genome of the species of said subject.

8. The method of Claim 6, further comprising providing an internal control and a non-amplifying oligonucleotide detection assay configured to detect said internal control, wherein said internal control target is detected using said non-amplifying oligonucleotide detection assay configured to detect said internal control.

9. A method for detecting aneuploidy of a chromosome in a subject, comprising the steps of:

a. selecting an exon tag sequence for said chromosome;

b. providing a non-amplified oligonucleotide detection assay configured to detect said exon tag sequence or its complement; and

c. detecting said exon tag with said non-amplified oligonucleotide detection assay.

10. The method of Claim 9, wherein said selecting an exon tag sequence comprises the steps of:

a. identifying a genic sequence that is specific to said chromosome in said subject, and that is unique in the genome of the species of said subject;

b. identifying an exon tag sequence within said genic sequence, wherein said exon tag sequence is compared to said genome to determine that said exon tag sequence is unique within said genome of the species of said subject.

11. The method of Claim 9, further comprising providing an internal control, and a non-amplifying oligonucleotide detection assay configured to detect said internal control, wherein said internal control target is detected using said non-amplifying oligonucleotide detection assay configured to detect said internal control.

12. The method of Claim 8 or Claim 11, wherein said internal control comprises a sequence from a gene on chromosome 1.

13. The method of Claim 6 or Claim 9, wherein said chromosome in a subject is selected from the group consisting of chromosomes 13, 18, 21, X and Y.

14. The method of Claim 6 or Claim 9 wherein said exon tag sequence is contained in a sample type selected from the group consisting of amniocyte cells, cystic hygroma fluid, amniocyte cell culture, amniotic fluid, chorionic villi, fetal urine, fetal skin, and fetal blood.

15. The method of Claim 14 wherein maternal nucleic acid is present as a contaminant in said sample.

16. The method of Claim 15 wherein maternal DNA comprises < about 80% of the total DNA isolated from said amniocyte cell culture.

17. A kit comprising a non-amplified oligonucleotide detection assay configured for detecting at least one exon tag.

18. The kit of Claim 17, wherein said non-amplified oligonucleotide detection assay comprises first and second oligonucleotides configured to form an invasive cleavage structure in combination with a target sequence comprising said at least one exon tag.

19. The kit of Claim 18, wherein said first oligonucleotide comprises a 5' portion and a 3' portion, wherein said 3' portion is configured to hybridize to said target sequence, and wherein said 5' portion is configured to not hybridize to said target sequence.

20. The kit of Claim 18, wherein said second oligonucleotide comprises a 5' portion and a 3' portion, wherein said 5' portion is configured to hybridize to said target sequence, and wherein said 3' portion is configured to not hybridize to said target sequence.

21. The kit of Claim 17, wherein said exon tag is from a gene selected from the group consisting of DSCR9, DLEU1, FLJ23403, PFKFB1, NRIP1, SRY, PCDH9, CN2, PRKY, HLCS, MTMR8, FLJ21174, and PCTK1.

22. The kit of Claim 17, further comprising an internal control.

23. The kit of Claim 22, wherein said internal control comprises a sequence from a gene on chromosome 1.